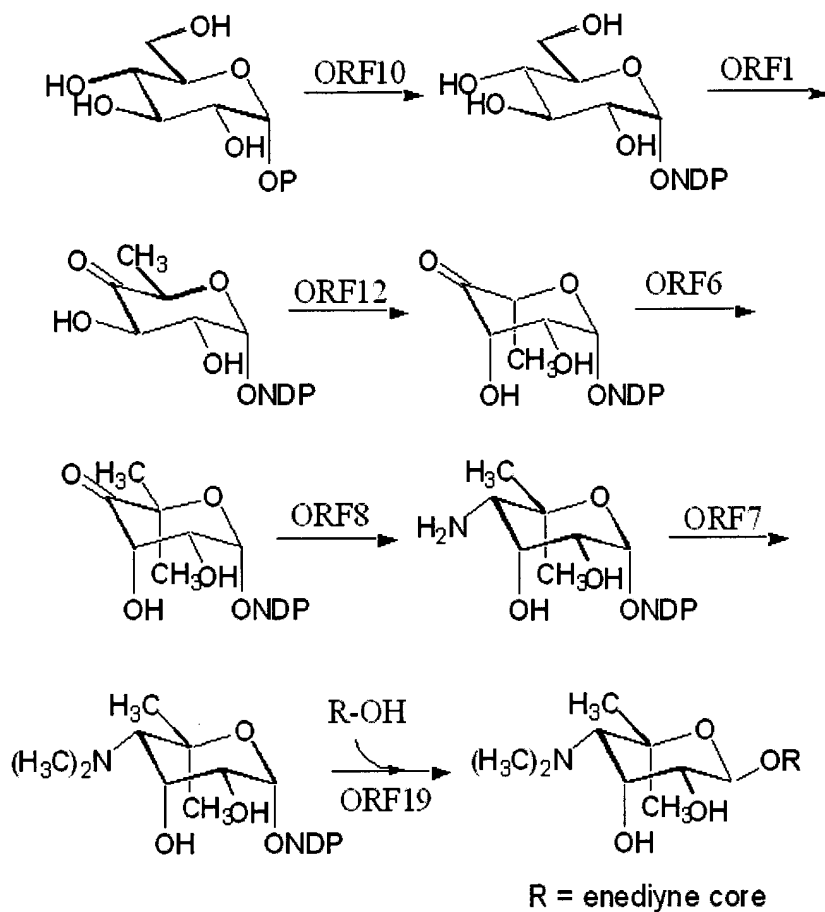


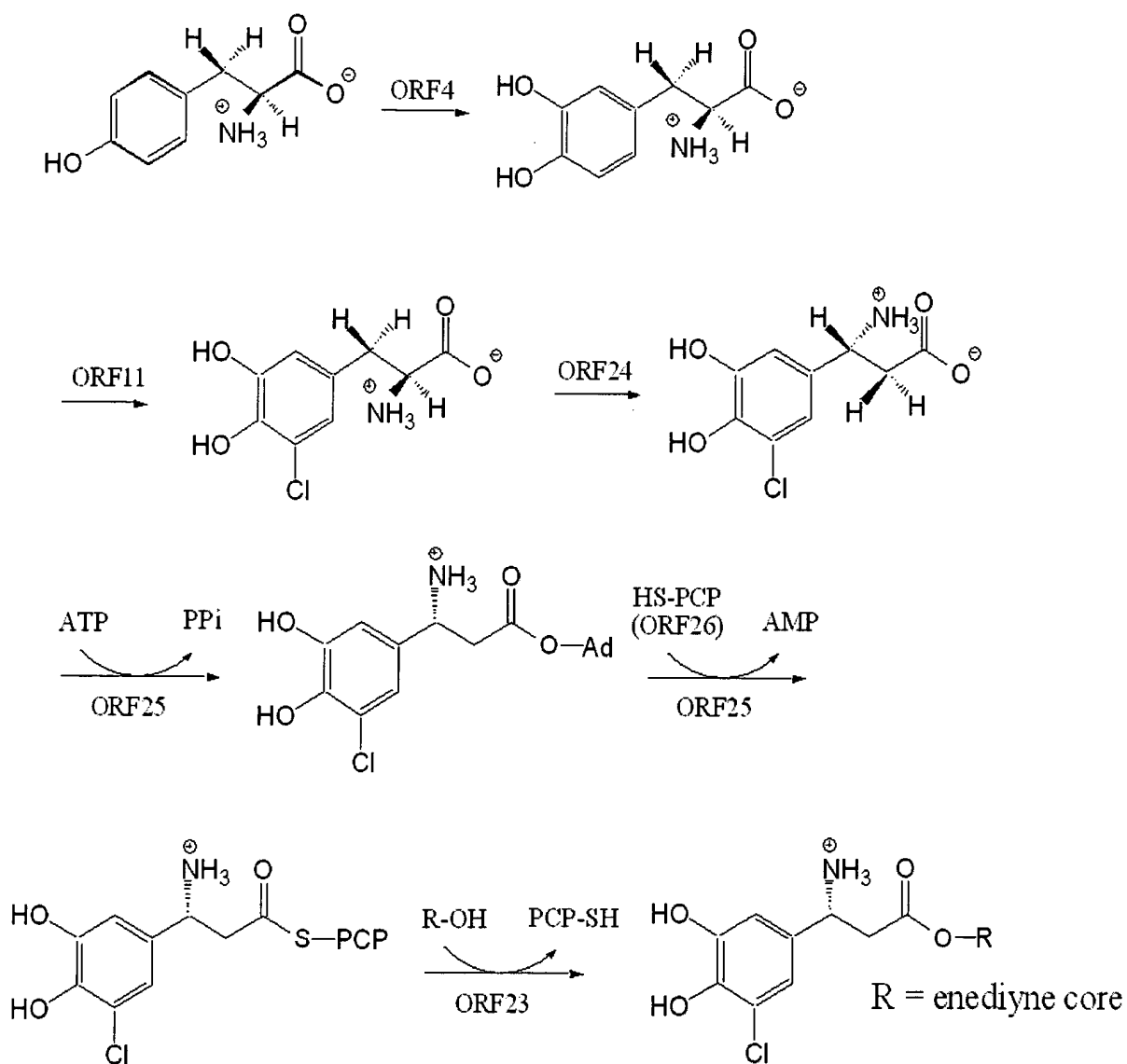
Fig. 1



ORF10: dNDP-glucose synthase, 355 aa
 ORF1: dNDP-glucose dehydratase, 332 aa
 ORF12: epimerase, 192 aa
 ORF8: aminotransferase, 410 aa

ORF6: C-methyltransferase, 423 aa
 ORF7: N-methyltransferase, 244 aa
 ORF19: glycosyl transferase, 459 aa

Fig. 2

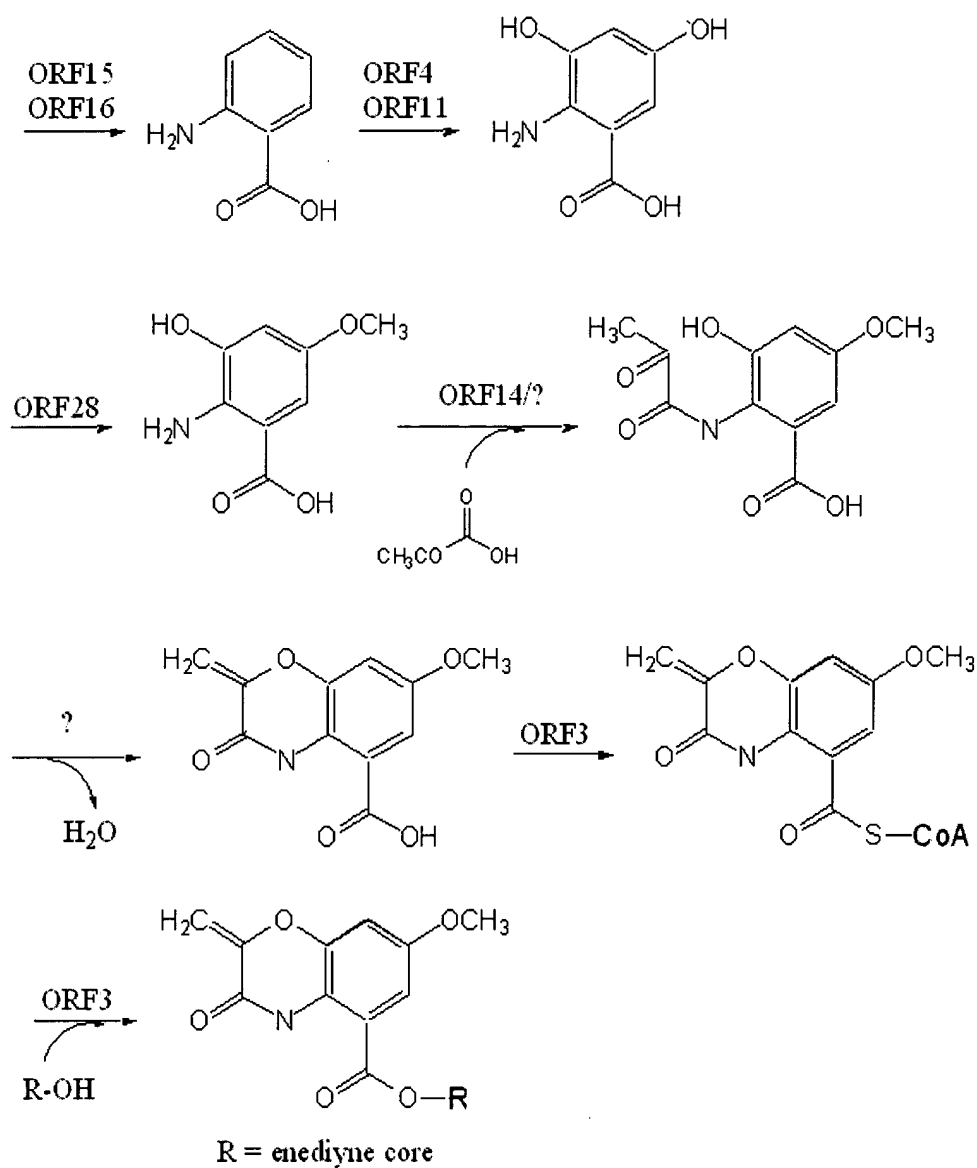


- ORF4:** Hydroxylase, 527 aa
ORF11: Hydroxylase halogenase, 492/494 aa
ORF24: Aminomutase, 539 aa
ORF23: Type II NRPS condensation enzyme, 459 aa
ORF25: Type II NRPS adenylation enzyme, 716 aa
ORF26: Type II peptidyl carrier protein 93 aa

Fig. 3A

10/15/02
 10/15/02

10/15/02
 10/15/02



ORF15: Anthranilate synthase I, 493 aa
ORF16: Anthranilate synthase II, 220 aa
ORF28: O-methyltransferase, 350 aa

ORF3: Coenzyme F390 synthetase, 463 aa
ORF14: Coenzyme F390 synthetase, 484 aa
ORF13: O-acyltransferase, 378 aa

Fig. 3B

ORF15: Anthranilate synthase I, 493 aa

ORF16: Anthranilate synthase II, 220 aa

Fig. 4

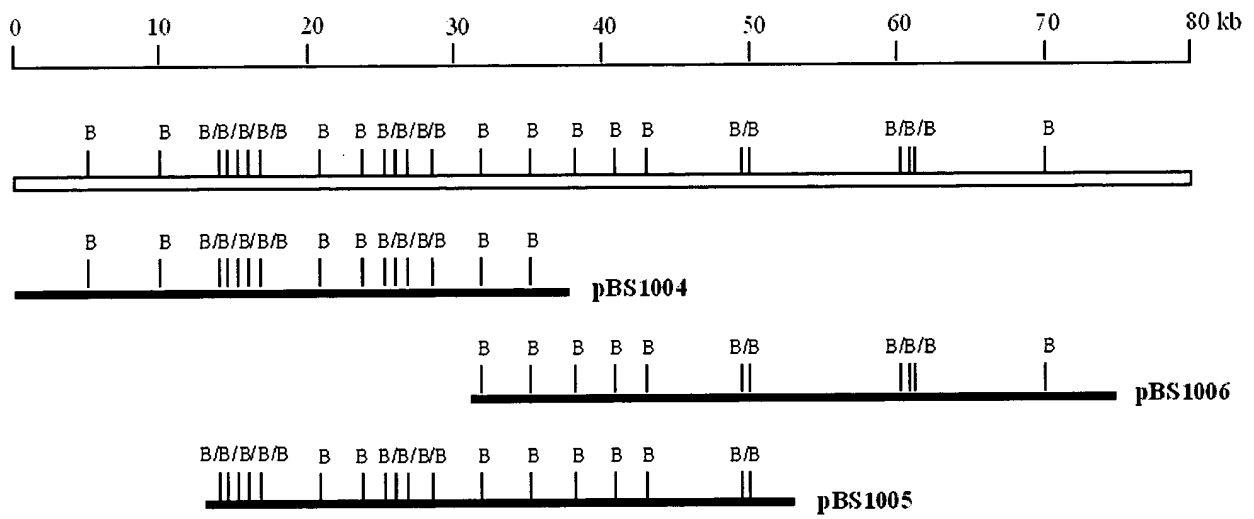


Fig. 5A

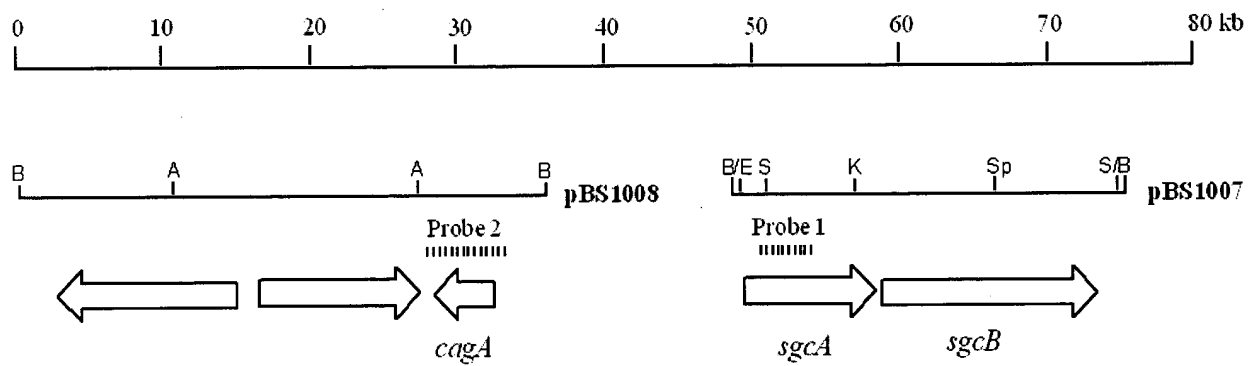


Fig. 5B

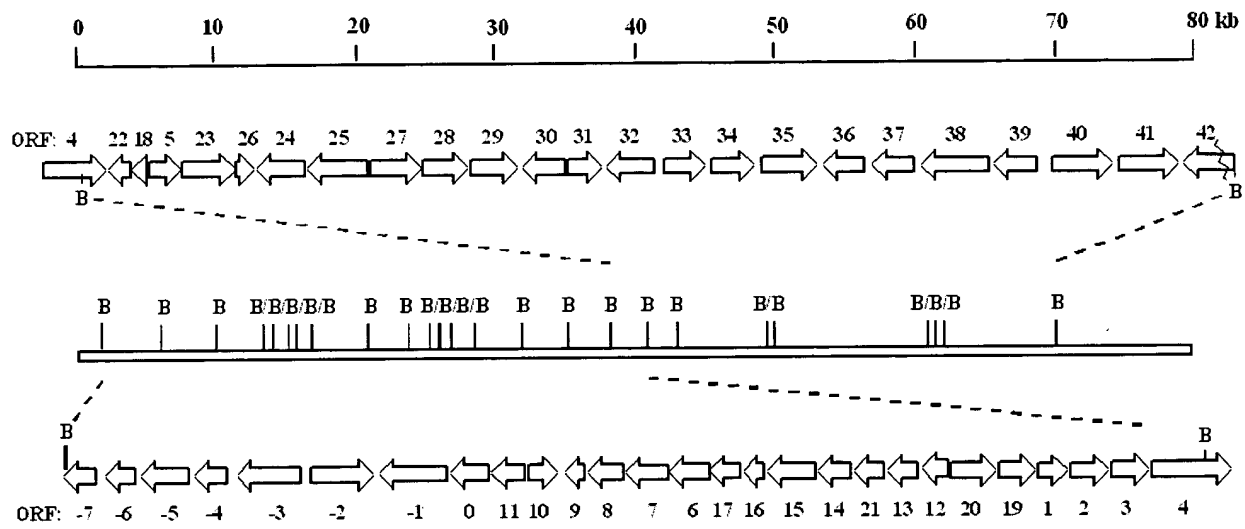


Fig. 5C



Gdh
TyLA2
SgcA
MtmE
consensus

1: ~ ~ ~ MRVLVTGGAGFIGSHYVRQLLGGAYPAFAFAGADV VLDKLTAYAGNEENLRPVADDERF: 57
1: ~ ~ ~ MRVLVTGGAGFIGSHFTGQLLTGAYEDDLGATRTV VLDKLTAYAGNPANLEHVAGHPDL: 57
1: ~ ~ ~ MRMLVTGGAGFIGSQFVRATLHGELEPG SEDARVT VLDKLTYSGNPANLTSVAAPRY: 57
1: MTTSILVTGGAGFIGSHYVRTLLGPR.. GVPDVT V VLDKLTAYAGTLTNLAEVSDSDRF: 58
1: mrVLVTGGAGFIGSHYVR LL g pa v VLDKLTAYaGn NL Va prf: 60

Gdh
TyLA2
SgcA
MtmE
consensus

58: RFVRGDI CEWDV VSEVVMREV DVVVFHAAET HVDRSIL GASDE VVTVNVVGTNTLLQ GAA: 117
58: EFVRGDIADHGWRRLMEGVGLVVFHAAESHVDRSIESSEAFVRTNVEGTRVLLQAAVDA: 117
58: TEVQGD TVDPRVDEVVAGHDVIVHFHAAESHVDRSIDTATRFTTNVLGTQTLLEAALRH: 117
59: RFVRGDI CDAPLVDLLAVHDQVVFHAAESHVDRSILGADEVR TNVTGTQTLLD AALRQ: 118
61: FVRGDI d vv evm dvvVFHAAESHVDRSI a EV TNV GTntLL aAL : 120

Gdh
TyLA2
SgcA
MtmE
consensus

118: NVSKFVHVSTDEVYGTIEHGSWPEDHLLEPNSPYSAAKAGSDLIARAYHRT HGLPVCITR: 177
118: GVGREVHI STDEVYGSIAEGSWPEDHPEVAPNSPYAATKAASDILLALAYHRT YGLDVRVTR: 177
118: GVGREVHVSTDEVYGSIAEGSWTEDTPLAPNPVYAAASKAGSDLMALAHRT RGLDVVTR: 177
119: GLETEVHI STDEVYGSIDA GSWPETAEVSPNSLYSAAKASDDLVALAYHRT HGLDVRVTR: 178
121: gv kFVHVSTDEVYGSi GSWpEd pl PNspY A KAgSDLiAlAYHRT hGLdV vTR: 180

Gdh
TyLA2
SgcA
MtmE
consensus

178: CSNNYGPYQFFPEKVLPLFTITNLMGRRR VPLYGDGLNVRDWLHVTDHCRGLIQLVAESGRAG: 237
178: CSNNYGPYQPEKAVPLFTITNLLDGLP VPLYGDGNTREWLHVD DHCGRVALV GAGGRPG: 237
178: CTNNYGPYQYPEKVIPLFVTNILLDGLR VPLYGDGAHRRDWLHVSDHCRATQMMN SGRAG: 237
179: CSNNYGS HQFFPEKVIPLFVTSLLDGRE VPLYGDGNTVRDWLHVDDHVRAIE LVRTGGRAG: 238
181: CSNNYGP QfPEKVIPLFiTnllDG VPLYGDG n RdWLHV DHcRgi lV GRAG: 240

Gdh
TyLA2
SgcA
MtmE
consensus

238: EITNIGGGTELTNKELTERTVLELMGQDWSMVQPVTDRKGHRRYSVDHTTKISEELGYEPV: 297
238: VITNIGGGTELTNAELTDRILELCCADRSALRRVADRP GHDRRY SVD TTKIRRELGYAPR: 297
238: EVYHIGGGTELSNEELTGLLLTA CGTDWSCVDRVADROGHDRRYSLDITKIROELGYEPL: 297
239: EVYHIGGGTELSNKELTQLLLDACCAGWDVRVYVTDKRGHRRYSVDCTKIRRELGYRPA: 298
241: eiYnIGGGTELTn ELT vle cg dws v V DR GHDRRYSVD TKIR ELGY P : 300

Gdh
TyLA2
SgcA
MtmE
consensus

298: VPFERGLAETIEWYRDNRRAWWEPLKSA PDGGK ~ ~ ~ : 329
298: TGITEGLAGTVAWYRDNRRAWWEPLKRSPG GRELERA: 333
298: VAFEDGLAATVKWYHENRSWQPLKEAAGLLDAVG ~ : 332
299: REF GDALAE TVAWYRHHRAWWEPL TRAYCAVAA ~ ~ ~ : 331
301: f egLA lV WYrdnRawWePlk a gg : 336

Fig. 7

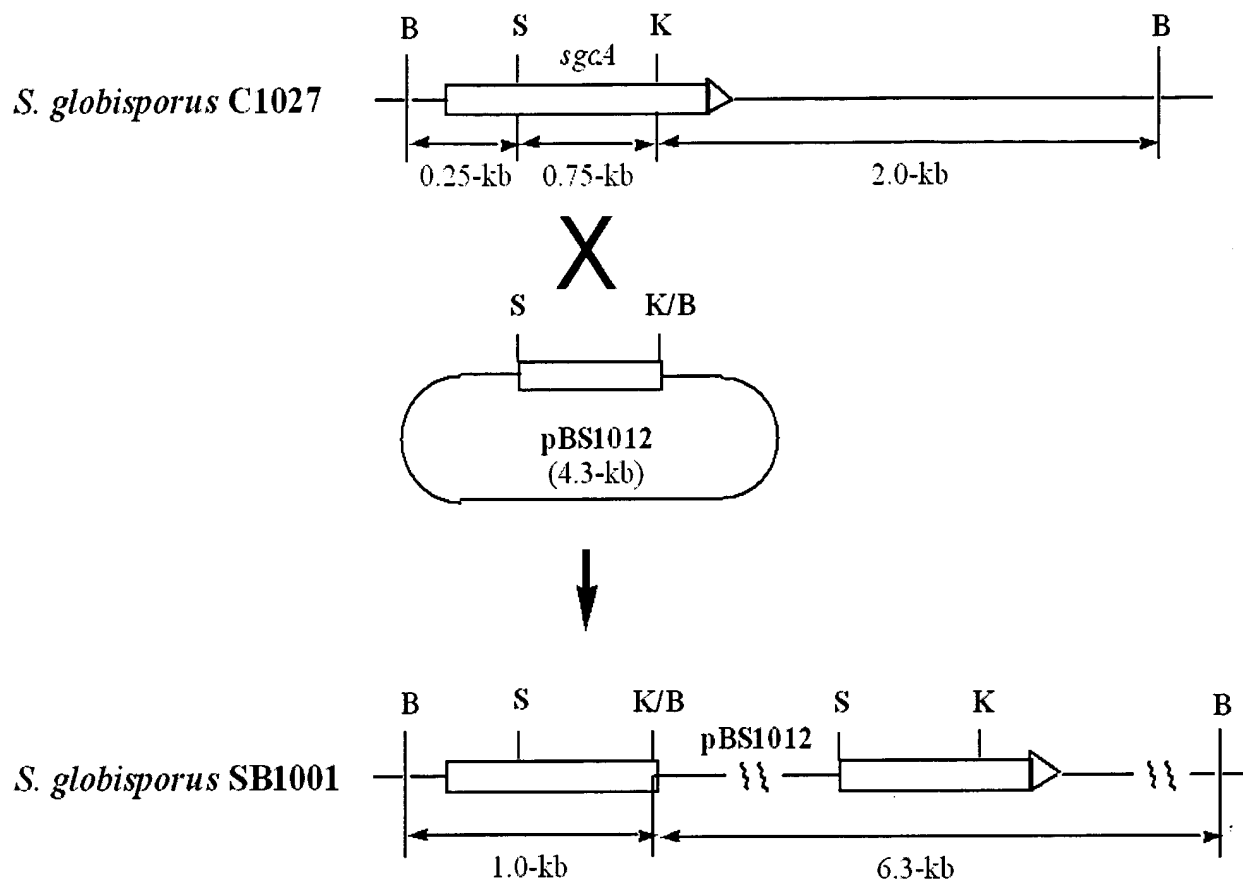


Fig. 8A

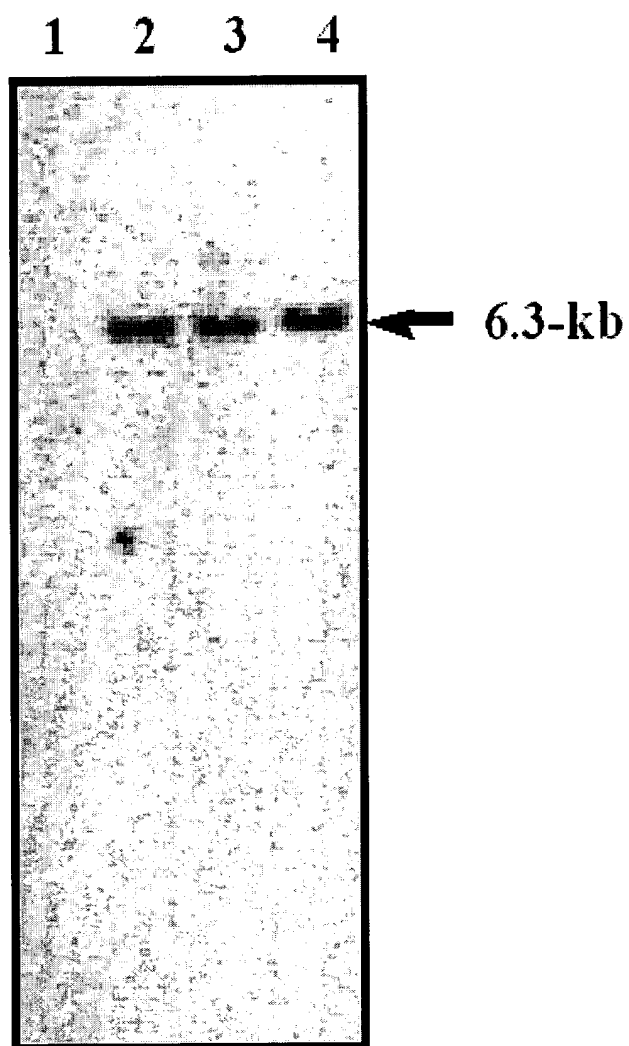


Fig. 8B

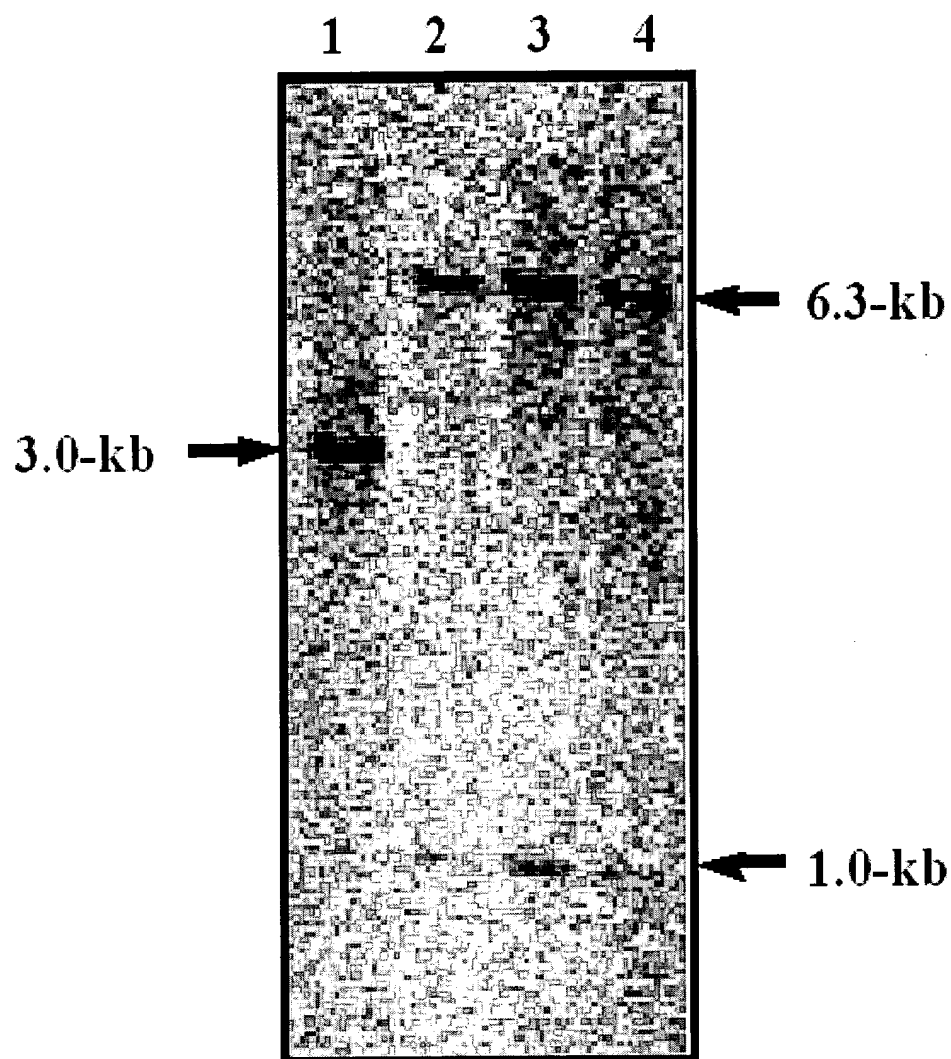


Fig. 8C

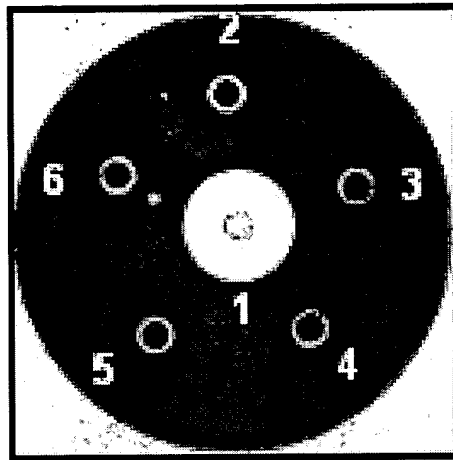


Fig. 9A

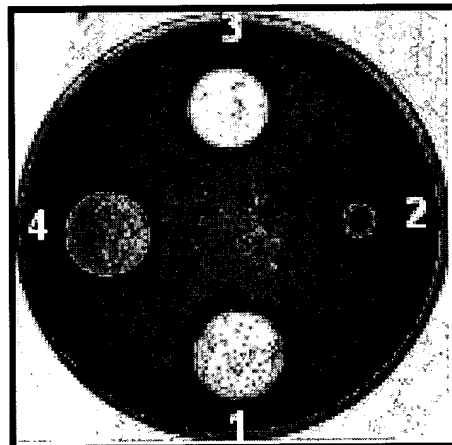


Fig. 9B

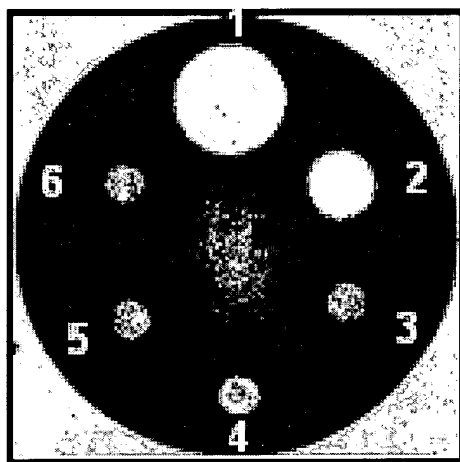


Fig. 9C

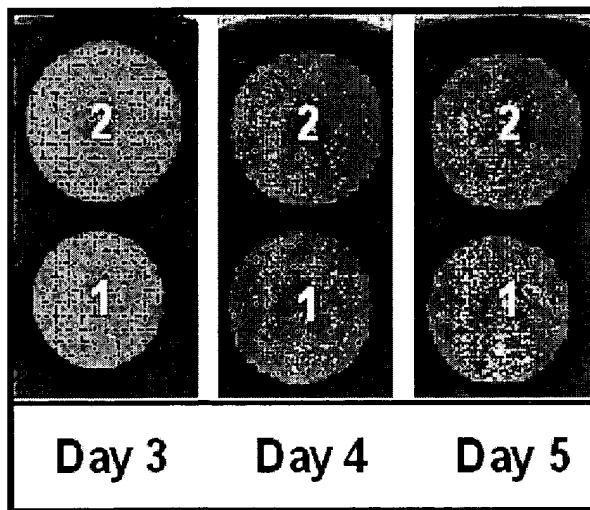


Fig. 9D

BamHI **EcoRI**

1 GGATCCGGGAAGACCGGAATTCGCCGCCAGCCCGTCTGAACCTCGTATCGCTCTGGTAGAAGCTGACGAAGCGTCAATCGCC GTGAC AAGGAGCGGACCG 100
sgca >

101 **ATG**AGGATGCTGGTGACGGGGGAGCGGGTTCATCGGCTCGCAGTTCGTGGGGCCACACTGCACGGCGAGCTGCCGGGTTCCGAGGACGCCCGGGTGA 200
 M R M L V T G G A G F I G S Q F V R A T L H G E L P G S E D A R V T

SacII

201 CGGTCTGGACAAGCTGACGTACTCCGGCAATCCGGCCAACTCACCTCCGTCCGGGCCCCATCCGGGTACACCTTCGTCCAGGGCGACACCGTCGACCC 300
 V L D K L T Y S G N P A N L T S V A A H P R Y T F V Q G D T V D P

301 GCGCGTCTGACGAGGTGGTCCGGCCGACGACGTATCGTCCACTTCGCGGGGAGTCGCACGTGGACCGCTCGATCGACACCGCCACCCGGTTCGTC 400
 R V V D E V A G H D V I V H F A A E S H V D R S I D T A T R F V

401 ACGACCAACGTGCTCGGACCCAGACGCTGCTGGAAGCGGCTCTCCGGCACGGGTTCGTGCACGTTCGACCGACGAGGTCTACGGGTCGA 500
 T T N V L G T Q T L L E A A L R H G V G R F V H V S T D E V Y G S I

501 TCGCCTCCGGCTCATGGACCGAGGACACCCCGCTCGCCGCCAACGTCCCTACGGCGGTTCGAAGCGGTTCGGACCTGATGGCGCTCGCCTGGCACCG 600
 A S G S W T E D T P L A P N V P Y A A S K A G S D L M A L A W H R

601 CACCCGGGGCTGGACGTGCTGTCACCCGGTGCACCAACAACACTACGGTCCCTACCACTACCCCGAGAAGGTGATCCCGTCTTCGTCAACCAACATCTC 700
 T R G L D V V T R C T N N Y G P Y Q Y P E K V I P L F V T N I L

701 GACGGCTTCGGGTGCCCTGTACGGGGACGGGCCACCCCGGGACTGGCTGCACGTTCGGACCACTGCCGGGCCATCCAGATGTCATGAATCCG 800
 D G L R V P L Y G D G A H R R D W L H V S D H C R A I Q M V M N S G

801 GCCGGCGGGGAGGTCTACCACTCGCGGGCGGACCGAATCTCCAACGAGGAATCAACGGCCCTGTGTCACGGCGTGGCGACCGACTGTCCTG 900
 R A G E V Y H I G G T E L S N E L T G L L T A C G T D W S C

901 CGTGGACCGGTGGCCGACCGGACGACCGCGCTACTCGCTCGACATCAAGAGATCCGGCAGGAATCGGGTACGAGCCCTGTCGCTTC 1000
 V D R V A D R Q G H D R R Y S L D I T K I R Q E L G Y E P L V A F

KpnI

1001 GAGGACGGCCTGGCCGACCGGTGAAGTGGTATCCACGAGAACCGTTCGTGGTGGCAGCCGCTGAAGGAAGCGGCCCGCCCTCCTGGACGCCCTCGGCTGAC 1100
 E D G L A A T V K W Y H E N R S W W Q P L K E A A G L L D A V G *

GAAAG

1101 GGCAGCCACCGCTAGGAACACCCACG GAGCCACCTCCGTGACAGCAGTCAAGGAGCCGACGTCCCGCAGGACGGCGGGAGTGGATCGCTCTCG 1200
sgcb > M T A V K E P T S R A G R R E W I A L V

1201 TCGTCTCTCTTGGCCACGATGCTGTTGATG CTGGACATCAACGTCTCATGTGGCCTTGCCGCAAGTTGAGCAGGATCTCGGCGGAGCAGCAGCA 1300
 V L S L P T M L L M L D I N V L M L A L P Q L S E D L G A S S T Q

1301 ACAGTGTGGATCACCAGACATCTACGGATTCCGGGCTTCCTGTTGACCATGGCACCCCTCGGACCGGATCGGCCCGCCAGGCTCTGCTC 1400
 Q L W I T D I Y G F A I A G F L V T M G T L G D R I G R R L L L

1401 GGGGGCGGGCGCTCTTCGGGTGCTGCTCGCGCTTCCTCGACAGCGGGCGATGCTGCTGTCAGCCCGCCGTGCTCGGCTCGCCGGG 1500
 G G A A V F A V V S V A A F S D S A A M L V V S R A V L G V A G A

1501 CCACGGTATGCCCTCGACGCTCGCGCTCATCAGCAACATGTTGAGGACCCCAAGGAGGGGACCGCCCATCGCCATGTGGCGAGCGCATGATGC 1600
 T V M P S T L A L I S N M F E D P K E R G T A I A M W A S A M A

1601 CGGAGTCGCCCTCGGGCCCGCGCTGCTCGCGCGCTGCTGTTCTCATCGCGGTTCGCGGTGATGCTGCTGCTG 1700
 G V A L G P A V G G L V L A A F W W G S V F L I A V P V M L L V V

Fig. 6



1701 GTCACGGCCCCGTGCTACCGAGTCCCGCGACCCCGGACGCCGCGGCTGACCTGACCGCGGGGCTCTCCCTCGCGACCGGTGCTGCCGGTGA
1800 V T G P V L L T E S R D P D A G R L D L L S A G L S L A T V L P V I
1801 TCTACGGACTGAAGGAGCTGGCCCCGAGACCGGGTGGGACCCGCTCGCGCGCGGTGCTCTCGCGCGGTGATCTTCGGCGCGGTGCTTCGTCAGCGCCA
1900 Y G L K E L A R T G W D P L A A G A V L G V I F G A L F V Q R Q
1901 GCGGGGTTGGCCGACCCCATGCTGGACCTCGGCCCTCTTCGCCGACCCGACCCCTCGCGGGCGGTCTGACGGTCACTGTGTTCAACGCCGTCATCATGGGC
2000 R R L A D P M L D L G L F A D R T L R A G L T V S L V N A V I M G

2001 GGGACCGGACTGATGGTCCGCTGTACCTCCAGACGATCGCCGGTCACTCCCGCTTGGCCCGCGGGCTGTGGCTGCTGATCCCGGCCCTGCATGCTCGTCG
2100 G T G L M V A L Y L Q T I A G H S P L A A G L W L I L I P A C M L V V
2101 TGGGCGTACAGTGTGGAACCTGCTGGCCCCAGGGATGCCCTTCCCGGTGCTGTGGGGGACTGCTGATCGCGCGGTGCGGACAGTCTCTGATCAC
2200 G V Q L S N L L A Q R M P P S R V L L G G L I A V G Q L L I T
2201 CCAGGTGGACACCGAGGACACCGCCCTCCTCATCGCGGCCACCACTGATCTACTTGGGCGCTCACCGGTGGGGCCGATCACCGGGCGGATCATG
2300 Q V D T E D T A L L I A A T T L I Y F G A S P V G P I T T G A I M
2301 GGAGCCGCCCCCGGAGAGGCGGTGCCCTCGTCTGTCGCCACCGCGCGGAGTTTCGGAGTGGCGCTCGGCATCGCGGGCTTGGGAGTCTGG
2400 G A A P P E K A G A S S L S A T G G E F G V A L G I A G L G S L G
2401 GCACCGTCTGTACAGCGCCGGGTCTGAGGTGCCGACCGCGCGGCCCGCGGACCGCGGACCGCGGAGAGCATCGCGGGCGCTGCACACGGC
2500 T V V Y S A G V E V P D A A G P A D A A Q E S I A G A L H T A
2501 CGGTCAGCTGGCACCGGGCAGCGCGACGCCCTGCTGGACTCCGCGCGCGGCTTACAGCGCGTGCAGTCCGCGCGCTGCGCGCGTGTTC
2600 G Q L A P G S A D A L L D S A R A A F T S G V Q S V A A V C A V F
2601 TCCCTGGCGCTCGCCGTCTCATCGGCACCCCGTCCGGGACATTTCCCGGATGGACCGGCGAGGAGAACCGCGGAGAACGACGCTCAACCGG
2700 S L A L A V L I G T R L R D I S A M D H G H G E P A E N D A Q P A
2701 CCACATGAGCGCACTTCCGGAGATGCAACGCGCGCCGTGAGGTATGAGGATCACCTTCCGGGGTGACCTGCACGGCAACGAGGCGGTAGTGGAGTACT
2800 T *
2801 GGAACAGCAGCGGAGACCATGCCCGCCAGGAACTCGAACAGTGGCGCAGGCTCCAGGCGGCCATGGACCGCACGCGCAGAAAGGCTTTCGCCCTT
2900 **SacII**
2901 CTGGCGGGAACGACTCCCCGAGAACATCACCTCCATGGCGGACTACGCGCGCGGGTGCCCTCTCTGCGCAAGGCCGACCTCTCTCGCGCGGAAAGCGCGG
3000 **BamHI**
3001 TCTCCCCCTTACGGCACCTGGCCCCCTCGCTGGATCC

Fig. 6 cont'd.

